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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on:

December 6, 2002, 19:53:16; Search time 2690 Seconds (without alignments) 16498.803 Million cell updates/sec

1 tctagaccatgtctggaaag......ccaactcagaagtagtcgac 1525 US-10-025-514-7 Perfect score: Seguence:

IDENTITY_NUC Gapox 1.0 Scoring table:

2054640 seqs, 14551402878 residues

4109280 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

GenEmbl:*

gb_ro:* gb_sts:* em_fun:* em_hum:* gb_ba:*
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is the number of results predicted by chance to have a Pred. No.

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

AR11110 Sequence 107949 Sequence 2 100556 Sequence 2 100559 Sequence 2 100559 Sequence 6 107947 Sequence 1 101252 Sequence 1 101227 Sequence 2 A01846 Human mRNA AN20208 Sequence 13616 Sequence 121616 Sequence 121616 Sequence 12 13616 Sequence 13 M32247 Rat alpha-1 S77822 alpha-1-ant D00675 Rat mRNA fo AB000546 ramias si E13268 Tamias asia X63129 B.taurus mR ARII1411 Sequence M11465 Human alpha E00631 DNA encodin I02706 Sequence 1 E00195 CDNA encodi 104196 Sequence 3 104272 Sequence 1 107849 Sequence 2 AX019486 Sequence AX335338 Sequence X01683 Human mRNA AK026174 Homo sap1 E00195 cDNA encod1 102398 Sequence 8 BC015642 Homo sap1 Af113676 Homo sap1 Af130068 Homo sapi BC011991 Homo sapi AX335339 Sequence K01396 Human alpha J02619 Human Z typ AR111412 Sequence Description SUMMARIES AF113676 AR111410 AF130068 HUMA1AT2 SSANTIELA RATATRA1 RATA1PI AB000546 E13268 136164 AX472008 AB000550 I01352 BABA1ATA AB004044 AX202089 BC015642 AX019486 AK026174 877822 Query Match Length DB Score 433.2 433.2 426.8 418.4 411.2 408.8 407.2 386.8 378 377.4 376.4 376.3 401.4 392.2 389

ALIGNMENTS

PAT 14-FEB-2001 M Unclassified.
Unclassified.
E 1 (bases 1 to 1308)
R Stilliff.T.D. and Rodriguez,R.L.
Production of .alpha. .sub.1 -antitrypsin in plants
AL Patent: US 6127145-A 6 03-0CT-2000;
Location/Qualifiers linear AR111412 1308 bp Sequence 6 from patent US 6127145. AR111412 AR111412.1 GI:12828260 Unknown. DEFINITION ACCESSION VERSION KEYWORDS ORGANISM AUTHORS TITLE JOURNAL FEATURES REFERENCE RESULT 1 AR111412

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                                                                 Length 1308;
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                                                                                    Pred. No. 2.1e-125;
0; Mismatches 346;
                                                                   41.3%; Score 630.4; DB 6; 70.8%; Pred. No. 2.1e-125;
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         /organism="unknown"
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                                                                         1415 TCCACCAGAAGTTAAATTTAATAAACCATTCGTTTTTCTGATGATGAGGAGAACACTAA 1474
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1295 TGTTACTGAAGAAGCTCCATTAAAATTGAGTAAAGCTGTTCACAAAGCCGTCTTAACTAT 1354
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Sutliff, T.D. and Rodriguez, R.L.
Production of alpha. .sub.1 -antitrypsin in plants
Patent: US 6127145-A 3 03-0CT-2000;
Location/Qualifiers
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70.8%; Pred. No. 3.4e-125;
tive 0; Mismatches 346;
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396 c 334 q
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59.9%; Pred. No. 5.8e
tive 0; Mismatches
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/db_xref="taxon:9606"
/map="14q32.1"
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/gene="PI"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRI 30-0CT-1994
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                                                                                                                                                                                        996 ATGAAAAGACTGGGTATGTTCAATATTCAACATTGCAAAAAATTAAGTTCTTGGGTCTTA 1055
                                                                                                                                                                                                                                                      1056 TTAATGAAGTATTAGGTAACGCTACTGCTATTTTTTTTTACCAGACGAAGGTAAGCTT 1115
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             876 GICTICGCACTAGITAACTATATITITICAAGGGTAAGTGGGAACGICCITICGAGGII
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Homo sapiens
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/translation="MPSSVSWGILLAGLCCLVPVSLAEDPQGDAAQKTDTSHHDQDHP
TFNKITPNLAEFAFSLYRQLAHQSNSTNIFFSPVSIATAFAMLSLGTKADTHDEILEG
LNFNLTEIPEAQIHEGFQELLRTLNQPDSQLQLTTGNGLFLSEGLKLVDKFLEDVKKL
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FREVKOPEDEDEHVDQYTYVKVPMMKLGKRFIDQHCKKLSSWYLLMATIGNATIFF
LPDEGKLQHLENBLITHDITYKFLENEDRRASSLHLPKLSITGTYDLKSVLGQTITK
FSNGADLSGVTEEAPLKLSKAVHKAVLTIDEKGTEAAGAMFLEAIPMSIPPEVKFNKP
[2] sites; alpha-1-antitrypsin deficiency disease mutations. The Granite Falls (a one base pair deletion), Bellingham (a substitution) and Mattawa (a one base pair insertion) mutations all result in premature transcription termination.

Location/Qualifiers
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Maagaretsuto, W.1. and Guren, H.K.
REGION SPECIFIC MUTATION INDUCTION IN ALPHA-1-ANTI-TRYPSIN PATENT. JP 1986012289-A 1 20-JAN-1986; CHIMO JIENETELTSUKUSU INCOS Muman
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PN JP 1986012289-A/1
PD 20-JAN-1986
PP 20-JAN-1986
PP 20-JAN-1985 JP 1985051553
PR 14-MAR-1984 US 84 589410, 07-MAR-1985 US 85 70
PR 14-MAR-1984 US 84 589410, 07-MAR-1985 US 85 70
C12N15/OO, AGIRSJ/74, AGIRSJ/74, AGIRSJ/74, AGIRSJ/74, AGIRSJ/74, AGIRSJ/74, AGIRSJ/764, CO7H21/04, CO7R15/04, PC
C12N21/OO, AGIRSJ/74, AGIRSJ/64, CO7H21/04, CO7R15/04, PC
C12N21/OO, AGIRSJ/74, AGIRSJ/64, CO7H21/04, CO7R15/04, PC
C12N21/OO, AGIRSJ/64, CO7H21/04, CO7R15/04, PC
C12N21/OO, AGIRSJ/64, CO7H21/04, CO7R15/04, PC
C C STANDGHORES BOCH;
CC ANDOCHACICAL: NO;
CC ANDOCHACICAL: NO;
CC ANDCORPER NO;
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.1193.'GCG')
/note='amino acid 358=Ala'
/note='amino acid 358=Val'
/note='amino acid 358=Val'
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/note='amino acid 342=Lys
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PAT 21-MAY-1993
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778 GTGATACTGAGGAAGCTAAAAAGCAAATTAATGATTATGTTGAGAAAGGCACCCAGGGTA 837
                                                                                      AGATCGTTGACCTAGTTAAAGAATTAGATCGTGATACCGTCTTCGCACTAGTTAACTATA 897
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1547 - 16th Ave. East; Seattle, WA
Location/Qualifiers
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Kawasaki, G.H.
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                                                                                                                                                                           62 TGGCAGGCCTGTGCTGCTGCTCCCTGGCTGAGGATCCCCAGGGAGATGCTG 121
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                                                                                 Length 1312;
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Homo sapiens, Similar to serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1, clone MGC:9222 IMAGE:3859644, mRNA, complete cds.
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Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,
A.M., Holloway, M., Telford, B, Hodgson, A., Bouck, J., Yu, W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 21 Row: d Column: 6
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 6855600.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1584)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (30-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
1258 ITACCAAAGTITITICTAACGGIGCCGAFTIGAGIGGIGTIACIGAAGAAGCICCATTAA 1317
                                                                                                                            1082 AGCTCTCCAAGGCCGTGCATAAGGCTGTGCTGACCATCGACGAGAAAGGGACTGAAGCTG 1141
                                                                                                                                                                                                                                                          AACCATTCGTTTTTCTGATGATCGAGCAGAACACTAAAAAGCCCATTGTTTATGGGTAAGG 1497
                                                                                                                                                                                                                                                                                     1022 TCACTAAGGTCTTCAGCAATGGGGCTGACCTCTCCGGGGTCACAGAGGAGGCACCCCTGA 1081
                                                                                    1318 AATTGAGTAAAGCTGTTCACAAAGCCGTCTTAACTATTGATGAAAAGGGTACCGAGGCCG 1377
                                                                                                                                                                        CCGGCGCTATGTTCCTGGAAGCTATTCCAATGAGCATTCCACCAGAAGTTAAATTTAATA 1437
                                                                                                                                                                                                cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL) DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
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/db_xref="taxon:9606"
/clone="MGC:9222 IMAGE:3859644"
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Tissue Procurement: DCTD/DTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: MGC help desk
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Direct Submission
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/codon_start=1 /product="Similar to serine (or cysteine) proteinase

/tissue_type="Ovary, adenocarcinoma" /clone_lib="NIH_MGC_66" /lab_host="DH10B"

/note="Vector: pCMV-SPORT6"

.1489

CDS

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GLNFNNITEIPEAQIHEGFOELLRTLNOPDSQLGTTGNGTFSBGLKTUVBKFLEDDYKK
ELYHSBATTVNFGDTEBEAKQINDYVEKGTQGKIVDLVKELDRDYVFALVNYIFFKGKW
ERPFEVKOTTEEBDFHVDQYTTVKVPMMKRLGHFNIQHCKKLSSMYLLMKYLGHATAIK
FLPDEGKLQHLBNELTHDIITKFLENERRSASLHLPKLSITGTYDLKSVLGQLGITK
VFSNGADLSGYTEEBAPIKLSKAVHKAVLTIDEKGTEAAGAMFLEAIPMSIPPEVKFNK
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inhibitor, clade A (alpha-1 antiproteinase, antitrypsin),
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                                                       /protein_id="AAH11991.1"
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Horrigan, S., Soppet, D.R. and Weaver, Z.
Cancer gene determination and therapeutic screening using signature
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Mammalia: Eutheria; Primates; Catarrhini, Hominidae, Homo.
1047 CCACCGCCATCTTCTTCCTGCCTGATGAGGGGAAACTACAGCACCTGGAAAATGAACTCA 1106
                                         1138 CTCATGACATTATTACTAAATTTTTAGAGAACGAGGATCGTCGTAGCGCTTCTCTGCACC 1197
                                                                                 TGCCAAAGTTAAGTATCACCGGTACTTACGACTTAAAATCTGTTTTAGGCCAGTTAGGTA 1257
                                                                                               1258 TTACCAAAGTTTTTTCTAACGGTGCCGATTTGAGTGGTGTTACTGAAGAAGCTCCATTAA 1317
                                                                                                                                                                  1227 TCACTAAGGTCTTCAGCAATGGGGCTGACCTCTCCGGGGTCACAGAAGGAGGCACCCTGA 1286
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Avalon Pharmaccuticals (US)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1258 TTACCAAAGTITITICTAACGGTGCCGATTIGAGTGGTGTTACTGAAGAAGCTCCATTAA 1317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AATTGAGTAAAGCTGTTCACAAAGCCGTCTTAACTATTGATGAAAAGGGTACCGAGGCCG 1377
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    538 CTAAAGCCGATACCCATGACGAGATTTTAGAAGGTTTAAACTTTAATTTGACCGAAATCC 597
                                                                                                                                                     598 CAGAAGCCCAAATTCACGAGGGTTTTCAAGAGTTGTTGAGAACTTTGAATCAACCTGATT 657
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                                                                                                                                                                                                                                                                                                                                718 ACAAATTCCTAGAAGACGTCAAGAAACTATATCATAGTGAGGCTTTTACCGTTAATTTTG 777
                                                                                                                                                                                                                                                                                                                                                                                                                     GTGATACTGAGGAAGCTAAAAAAGCAAATTAATGATTATGTTGAGAAAGGCACCCAGGGTA 837
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ptrnkitepreapchtVQCTVCKPWAKKTSKNVKELDRPTVRFLUMY TFRGKW
LYHSEAFTVNFGDTEEAKOINDYVEKGTGCKIVDLYKELDRPTVAKYLGNTATFFRGKW
ERPPERKLOHLENELTHDIITKFLENEDRRGASHLHCKLSTTGTYDLKSVLGNATAIF
FLPDEGKLQHLENELTHDIITKFLENEDRRGASHLHCKLSTTGTYDLKSVLGOLGITK
VFSNGADLSGYTEEAPLKKAVHKAVLTIDEKGTEAAGAMFLEAIPMSIPPEVKFNK
PPVFLMIEQNIKSPLEMGKVVNPTQK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alpha-1-antitrypsin is synthesized in the liver and is a major Alpha-1-antitrypsin is synthesized in the liver of elastase, constituent of plasma. It functions as an inhibitor of elastase, which degrades lung tissues. Hereditary deficiencies are fairly frequent, causing early lung degeneration and sometimes severe liver disorders. Defectives are particularly sensitive to pollution induced inflammation. Injection of anti-trypsin relieves the condition [1].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 1352)
Colau,B., Chuchana,P. and Bollen,A.
Revised sequence of full-length complementary DNA coding for human
           PRI 01-NOV-1994
                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1231)

1 (bases 1 to 1231)

1 (bases 1 to 1231)

2 (bases 2 to 1231)

2 (bases 3 to 1231)

3 (bases 1 to 1231)

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                                                                                                                                                               alpha-1-antitrypsin; antiprotease; antitrypsin.
Human liyer, cDNA to mRNA, clones pULB1523 [1] and pTG603 [3]
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                  linear
                      Human alpha-1-antitrypsin mRNA, complete cds.
K01396
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20. .1276
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="14q32.1"
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DNA 3 (4), 327-330 (1984)
85026667
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Pred. No. 5.6e-83;
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es 493; Indels
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799. .802
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/citation=[1]
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Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G., Horrigan, S., Soppet, D.R. and Weaver, Z. Cancer gene determination and therapeutic screening using signature
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898 TTTTTTTCAAGGGTAAGTGGGAACGTCCTTTCGAGGTTAAAGATACTGAAGAGAAGATT 957
                   774 ACAICCAGCACTGTAAGAAGCTGTCCAGCTGGGTGCTGCTGAATACCTGGGCAATG
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PTRKTTPRAAFSITYGLAHQSWTRIFFSPSYSYATAFAALSLGFAATHDELLE
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BEPFEWVGTEEBEPHVDQTYTWYPWARKRAGMFNIOHGKKKKKSWTLAKKICKSMTRF
FLPDFGKLQHLENDFITYRFLENDPRASASLHLPKLSTTGTYDLKSYLGQLGTTK
VFSNGAALSGYTEEAHLKLSKRAVHKAVLITDEKGTEAAGAMFLEAIFWSIPPEVKFNK
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I (bases 1 to 274)
Kurachi, K., Chandra, T., Degen, S.J., White, T.T., Marchioro, T.L., Woo, S.L. and Davie, E.W.
Cloning and sequence of cDNA coding for alpha 1-antitrypsin Proc. Natl. Acad. Sci. U.S.A. 78 (11), 6826-6830 (1981)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bollen, A., Herzog, A., Cravador, A., Herlon, P., Chuchana, P., Vander Straten, A., Loriau, R., Jacobs, P. and van Elsen, A. Cloning and expression in Escherichia coli of full-length complementary DNA coding for human alpha 1-antitrypsin B4107980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rosenberg, S., Barr, P.J., Najarian, R.C. and Hallewell, R.A.
Synthesis in yeast of a functional oxidation-resistant mutant of
human alpha-antitrypsin
Nature 312 (5989), 77-80 (1984)
                      1378 CCGGCGCTATGTTCCTGGAAGCTATTCCAATGAGCATTCCACCAGAAGTTAAATTTAATA 1437
                                                                                   1438 AACCATTCGTTTTTCTGATGATCGAGCAGAACACTAAAAGCCCATTGTTTATGGGTAAGG 1497
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/protein_id="CAA25838.1"
/db_xref="G1:28966"
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                                                                                                                                                                                                                                                                                                                                              Human mRNA for alpha 1-antitrypsin.
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Colau, B., Chuchana, P.
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JOURNAL MEDLINE

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JOURNAL MEDLINE

CDS

FEATURES

MEDLINE

JOURNAL

ORGANISM

KEYWORDS

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RESULT 10 HSATPR1

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958 IICAIGIIGAICAAGIIACIACIGICAAAGIICCAAIGAIGAAAAGACIGGGIAIGIICA 1017
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Pred. No. 5.5e-83;
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Matches 729; Conservative
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AKO26174 11399 bp mRNA linear PRI 29-SEP-2000 Homo sapiens cDNA: FLJ22521 fis, clone HRC12386, highly similar to AFI13676 Homo sapiens clone FLB2803 PRO0684 mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (29-A0G-2000) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center: Shirokane-dal, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Pax:81-3-5449-5416)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo Sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Manmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kawabata, A., Hikiji, T., Kobatake, N., Inagaki, H., Ikema, Y., Okamco, S., Okitani, R., Ota, T., Suzuki, Y., Obayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Nakamura, Y., Isogai, T. and Sugano, S. NEDO, human CDNA sequencing project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Blottechnology; cDNA library construction, 5'- & 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology
1258 TTACCAAAGTTTTTTCTAACGGTGCCGATTTGAGTGGTGTTACTGAAGAAGCTCCATTAA 1317
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Shibahara, T., Tanaka, T. and Nakamura, Y.
Direct Submission
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Homo sapiens primary human renal epithelial cells cDNA to mRNA,
clone_lib:HRC clone:HRC12386.
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/cell_type="primary human renal epithelial cells"
/clone_lib="HRC"
/note="cloning vector pME18SFL3"
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/db_xref="taxon:9606"
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 Length 1399;
                                   Indels
 Score 433.2; DB 9;
Pred. No. 5.5e-83;
0; Mismatches 493;
28.4%;
59.7%;
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                                                             1158 CIGGGGCCAIGTITIAGAGGCCATACCCATGTCTATCCCCCCGAGGTCAAGTTCAACA 1217
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grant, R. and Richiyaado, U.
SUGAR LYSING PROMOTOR: PROTEASE INHIBITOR FOR DEVELOPMENT
ADJUSTED PROTEIN
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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I (bases 1 to 1134)
Parker,M.L. and Kawasaki,G.H.
Method of expressing alpha-1-antitrypsin in bacteria and its use in therapeutic formulations, and vectors and bacteria for such method and their productions, and vectors and bacteria for such method Patent: EP 0137633-A1 3 17-APR-1985;
Location/Qualifiers
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Patent: EP 0139383-A1 1 02-MAY-1985;
                                       1018 ATATTCAACATTGCAAAAAATTAAGTTCTTGGGTCTTATTAATGAAGTATTTAGGTAACG 1077
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Russell, P.R.
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Kawasaki, G.H. and Woodbury, R.G.
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